

LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression

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ABSTRACT

Long non-coding RNAs (lncRNAs) have emerged as critical regulators of genes at epigenetic, transcriptional and post-transcriptional levels, yet what genes are regulated by a specific lncRNA remains to be characterized. To assess the effects of the lncRNA on gene expression, an increasing number of researchers profiled the genome-wide or individual gene expression level change after knocking down or overexpressing the lncRNA. Herein, we describe a curated database named *LncRNA2Target*, which stores lncRNA-to-target genes and is publicly accessible at <http://www.lncrna2target.org>. A gene was considered as a target of a lncRNA if it is differentially expressed after the lncRNA knockdown or overexpression. *LncRNA2Target* provides a web interface through which its users can search for the targets of a particular lncRNA or for the lncRNAs that target a particular gene. Both search types are performed either by browsing a provided catalog of lncRNA names or by inserting lncRNA/target gene IDs/names in a search box.

INTRODUCTION

A large number of long non-coding RNAs (lncRNAs) have been identified (1), and emerging studies have revealed that lncRNAs are not transcriptional noise but play important roles in the regulation of a wide range of processes (2,3) and diseases (4–7). To help researchers to better understand lncRNAs, many important lncRNA databases have been

developed. For example, Chen *et al.* developed a beneficial database named ‘LncRNADisease’ that store experimentally verified lncRNA–disease associations (6); Amaral *et al.* developed a wonderful database named ‘lncRNADB’ that contains a comprehensive list of lncRNAs that have been shown to have, or to be associated with, biological functions in eukaryotes (8); Volders *et al.* constructed a helpful database titled ‘LNCipedia’ for the annotation of human lncRNA transcript sequences and structures (9); Yang *et al.* described a valuable database ‘ChIPBase’ to facilitate the comprehensive annotation and discovery of transcription factor binding maps and transcriptional regulatory relationships of lncRNAs from ChIP-Seq data.

Many studies have demonstrated that lncRNAs play crucial roles in the regulation of gene expression at epigenetic (10), transcriptional (11) and post-transcriptional (12) level. Recently, using low-throughput experimental technologies (e.g. quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR) and western blot) and high-throughput experimental technologies (e.g. microarray or RNA-seq), an increasing number of researchers have attempted to profile the individual or genome-wide gene expression level change after knocking down or overexpressing a lncRNA of interest, and identified the differentially expressed genes as the target genes of the lncRNA for further functional analysis of the lncRNA. However, detailed information on these lncRNA–target relationships are scattered in relevant literature and there is no online repository that stores the information.

To fill this gap, we considered target genes of a lncRNA as the differentially expressed genes after knocking down or overexpressing the lncRNA, and developed a database named *LncRNA2Target* to manage all experimentally ver-

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Disclaimer: In our database, all differentially expressed genes after lncRNA perturbation were considered as targets of the lncRNA. Although this indeed suggests downstream regulation, it is no real proof of direct interaction. The effects on expression may be secondary or tertiary.

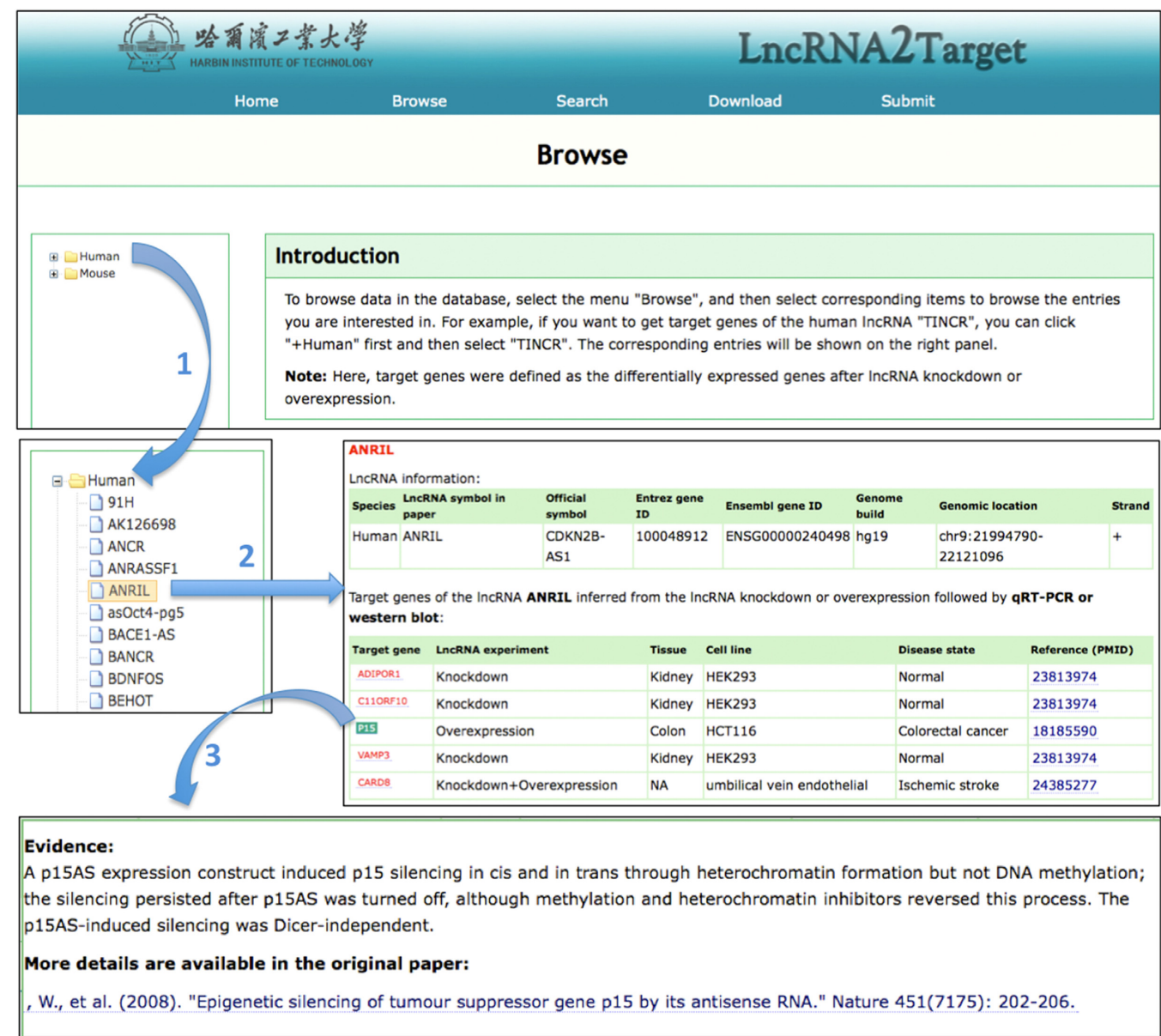


Figure 1. Screenshot of how to browse the target genes of lncRNA 'ANRIL'.

Table 1. LncRNA knockdown or overexpression experiments followed by qRT-PCR or western blot to identify differentially expressed target genes

	No. of lncRNAs	No. of target genes	No. of lncRNA-target associations
Human	68	216	278
Mouse	26	95	118

Table 2. LncRNA knockdown or overexpression experiments followed by microarray or RNA-seq to identify differentially expressed target genes

	No. of lncRNAs	No. of target genes	No. of lncRNA-target associations
Human	14	11 389	26 133
Mouse	109	14 667	67 034

LncRNA2Target

Home Browse Search Download Submit

Search

LncRNA-Target

Species: Target genes of a lncRNA are defined as the differentially expressed genes after lncRNA knockdown or overexpression.

Input type: • Users can obtain the target genes affected by a lncRNA by searching the lncRNA entrez gene ID or symbol

Fuzzy search: • Users can obtain the regulatory lncRNAs of a specific target gene by searching the target entrez gene ID or symbol

Submit

Examples: Target gene: **CDKN1A**; LncRNA: **HOTAIR**

retrieve target genes by lncRNA

retrieve lncRNAs by target gene

Result 1: CDKN1A

CDKN1A is differentially expressed after knocking down or overexpressing each of the following 6 lncRNA(s):

The differentially expressed **CDKN1A** (also known as **P21**) was inferred from the lncRNA knockdown or overexpression experiment followed by qRT-PCR or western blot:

LncRNA symbol	LncRNA entrez ID	LncRNA experiment	Reference	Details
HEIH	100859930	Knockdown+Overexpression	Yang, F., et al. (2011). "Long noncoding RNA high expression in hepatocellular carcinoma facilitates tumor growth through enhancer of zeste homolog 2 in humans." Hepatology 54(5): 1679-1689.	show details
HOTAIR	100124700	Knockdown+Overexpression	Liu, Z., et al. (2013). "The long noncoding RNA HOTAIR contributes to cisplatin resistance of human lung adenocarcinoma cells via downregulation of p21(WAF1/CIP1) expression." PLoS One 8(10): e77293.	show details
UCA1	652995	Knockdown+Overexpression	Wang, X., et al. (2014). "Long non-coding RNA urothelial carcinoma associated 1 induces cell replication by inhibiting BRG1 in 5637 cells." Oncol Rep.	show details

Evidence:

Analysis with RT-PCR and western blotting confirmed that the expression of PRC2 target genes, such as the cell-cycle regulation genes, p15, p16, p21 and p57 were diminished when lncRNA-HEIH was overexpressed and up-regulated when lncRNA-HEIH was knocked down. lncRNA-HEIH plays a key role in G(0)/G(1) arrest, and further demonstrated that lncRNA-HEIH was associated with enhancer of zeste homolog 2 (EZH2) and that this association was required for the repression of EZH2 target genes.

Experiment information on HEIH:

Species: Human
LncRNA name: HEIH
Official symbol: HEIH
Entrez ID: 100859930
Ensembl ID: NA
Genome build: hg19
Location: chr5:180256954-180258618
Strand: -

Result 1: HOTAIR

LncRNA Information:

Species	LncRNA symbol in paper	Official symbol	Entrez gene ID	Ensembl gene ID	Genome build	Genomic location	Strand
Human	HOTAIR	HOTAIR	100124700	ENSG00000228630	hg19	chr12:54356092-54368740	-

Target genes of the lncRNA **HOTAIR** inferred from lncRNA knockdown or overexpression followed by qRT-PCR or western blot:

Target gene	LncRNA experiment	Tissue	Cell line	Disease state	Reference (PMID)
HOTAIR	Knockdown+Overexpression	Lung	A549, SPC-A1, NCI-H1975	Non-small cell lung cancer (NSCLC)	24103700
MMP3	Knockdown+Overexpression	Stomach	AGS and SGC-7901	Gastric cancer (GC)	23847441
MMP3	Knockdown+Overexpression	Stomach	AGS and SGC-7901	Gastric cancer (GC)	23847441
MMP3	Knockdown	Liver	Bel7402	Hepatocellular carcinoma (HCC)	22289527

Evidence:

The expression level of HOTAIR in cancer tissues was higher than that in adjacent noncancerous tissues. Expression level of HOTAIR was significantly correlated with lymph node metastasis and TNM stage. Furthermore, high expression level of HOTAIR was a predictor of poor over-all survival in GC patients. In vitro, inhibition of HOTAIR in GC cells could reduce invasiveness, as well as the expression of MMP1 and MMP3. In addition, suppression of HOTAIR could reverse EMT process.

More details are available in the original paper:

Xu, Z. Y., et al. (2013). "Knockdown of long non-coding RNA HOTAIR suppresses tumor invasion and reverses epithelial-mesenchymal transition in gastric cancer." Int J Biol Sci 9(6): 587-597.

Figure 2. Screenshot of how to search target genes of lncRNA of interest or all lncRNAs that regulate a specific target gene.

ified lncRNA-target associations that were curated from published papers and microarray and RNA-seq data sets. Our database not only facilitates computational investigators to perform integrative analysis of the publicly available lncRNA targets but also enables experimental scientists to analyze their own data in the context of other related public data.

DATABASE OVERVIEW

The *LncRNA2Target* knowledge base aims to facilitate users to browse, search and download all literature-based lncRNA-target associations in the database, and submit novel data to the database. To extract the experimentally supported lncRNA-target associations, we first got all lncRNA papers published before 30 July 2014 by searching the PubMed literature database with keywords 'lncRNA', 'lincRNA', 'long non-coding RNA' or 'long intergenic non-coding RNA', respectively. Then, information on lncRNA-target associations was retrieved from the 150 papers and 11 high-throughput public data sets. Every association contains 18 items, such as species, lncRNA symbol/ID/location/strand, cell line in which the lncRNA knockdown or overexpression experiments was performed,

disease state, target gene symbol/ID, supporting evidence for the lncRNA-target association and reference information. The detailed statistics on lncRNA-target associations are shown in Tables 1 and 2.

DATABASE ACCESS

User-friendly web interface was developed to facilitate users to browse, search and download the lncRNA-target association data, and upload new experientially verified lncRNA-target association to the database. Once approved by the submission review committee, the submitted record will be included in the database, and made available to the public in the coming release.

Browsing the database

Data in *LncRNA2Target* database can be browsed by lncRNA symbol. To browse the data, users first go into the 'Browse' page, and then select a species and a lncRNA they are interested in. For example, if the user wants to get target genes of the human lncRNA 'INRIL', you can click '+Human' first and then select 'INRIL'. The corresponding entries will be shown on the right panel. In this panel, basic

lncRNA information are shown, such as lncRNA symbol used in the original paper, official lncRNA symbol, its entrez or Ensembl gene ID, genomic location, strand, etc. In addition, the target genes of the lncRNA, cell line in which the lncRNA knockdown/overexpression experiments was performed, disease state and reference information are also shown in this panel. When users click the target symbol, a new window will be popped up, where the experimental evidence for supporting the lncRNA-target association is shown. An example on how to get the target genes of lncRNA 'INRIL' is shown in the Figure 1.

Searching the database

The LncRNA2Target database provides a 'Search' function for users to retrieve the lncRNA-target associations by lncRNA or target gene. The 'Search' is case-insensitive. Users can obtain the target genes affected by a lncRNA by searching the lncRNA entrez gene ID or symbol, and also can obtain the regulatory lncRNAs of a specific target gene by searching the target entrez gene ID or symbol. An example on how to retrieve the lncRNAs that regulate a specific gene named 'CDKN1A' and how to retrieve the target genes of lncRNA named 'HOTAIR' is shown Figure 2.

FUTURE DEVELOPMENT

As the number of lncRNA knockdown/overexpression experiments followed by qRT-PCR, western blot, microarray or RNA-seq to identify differential target genes increases exponentially, a submission page allows researchers to inform us about new publicly available data by inputting a PubMed ID or GEO accession. After manual curation and computational analysis, the new lncRNA target genes will be accessible in the coming release. In addition, we will search the PubMed and GEO database for extracting new available lncRNA-target associations, and update the LncRNA2Target regularly. With the joint effort between our lab and the lncRNA community, the LncRNA2Target will be a valuable resource for the lncRNA community.

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